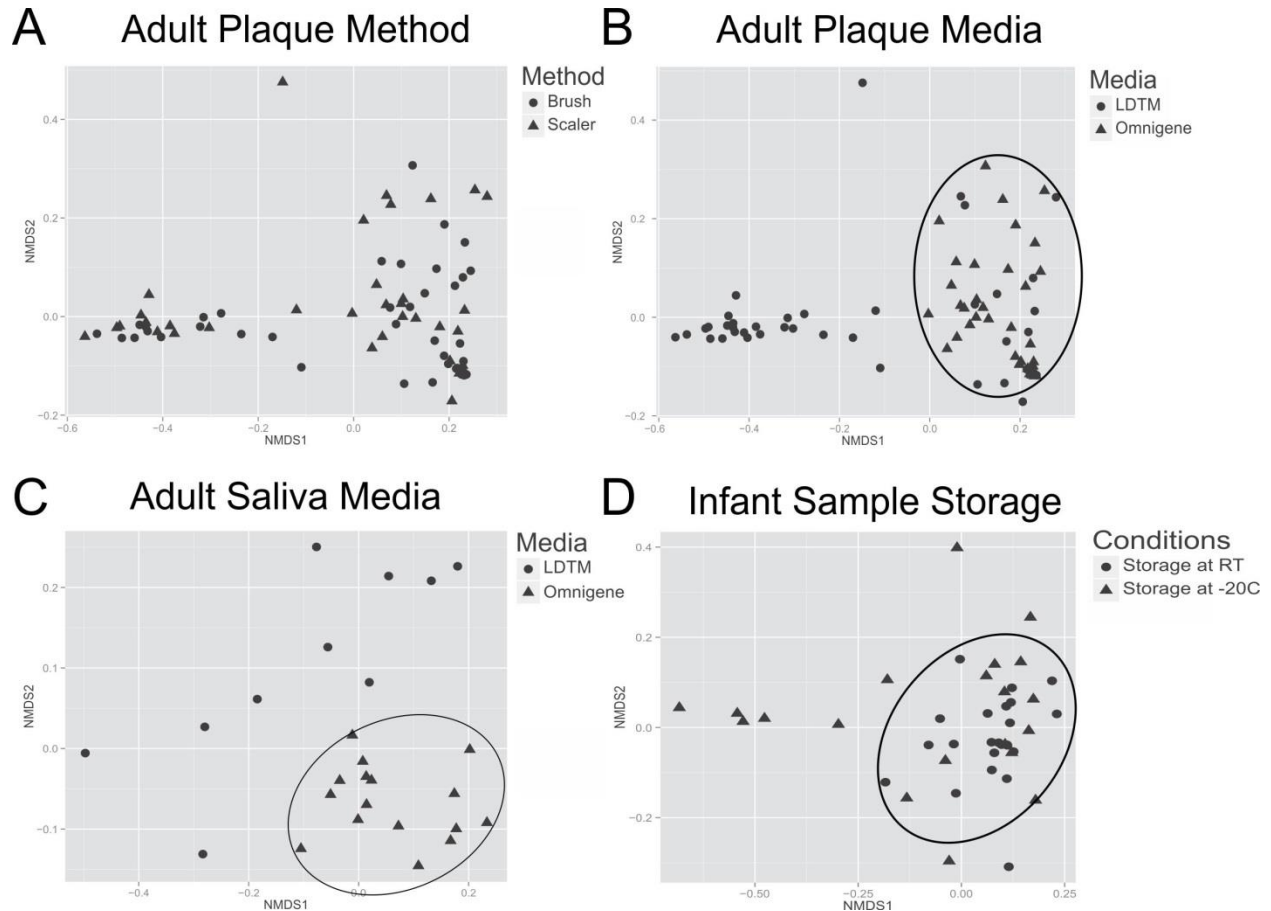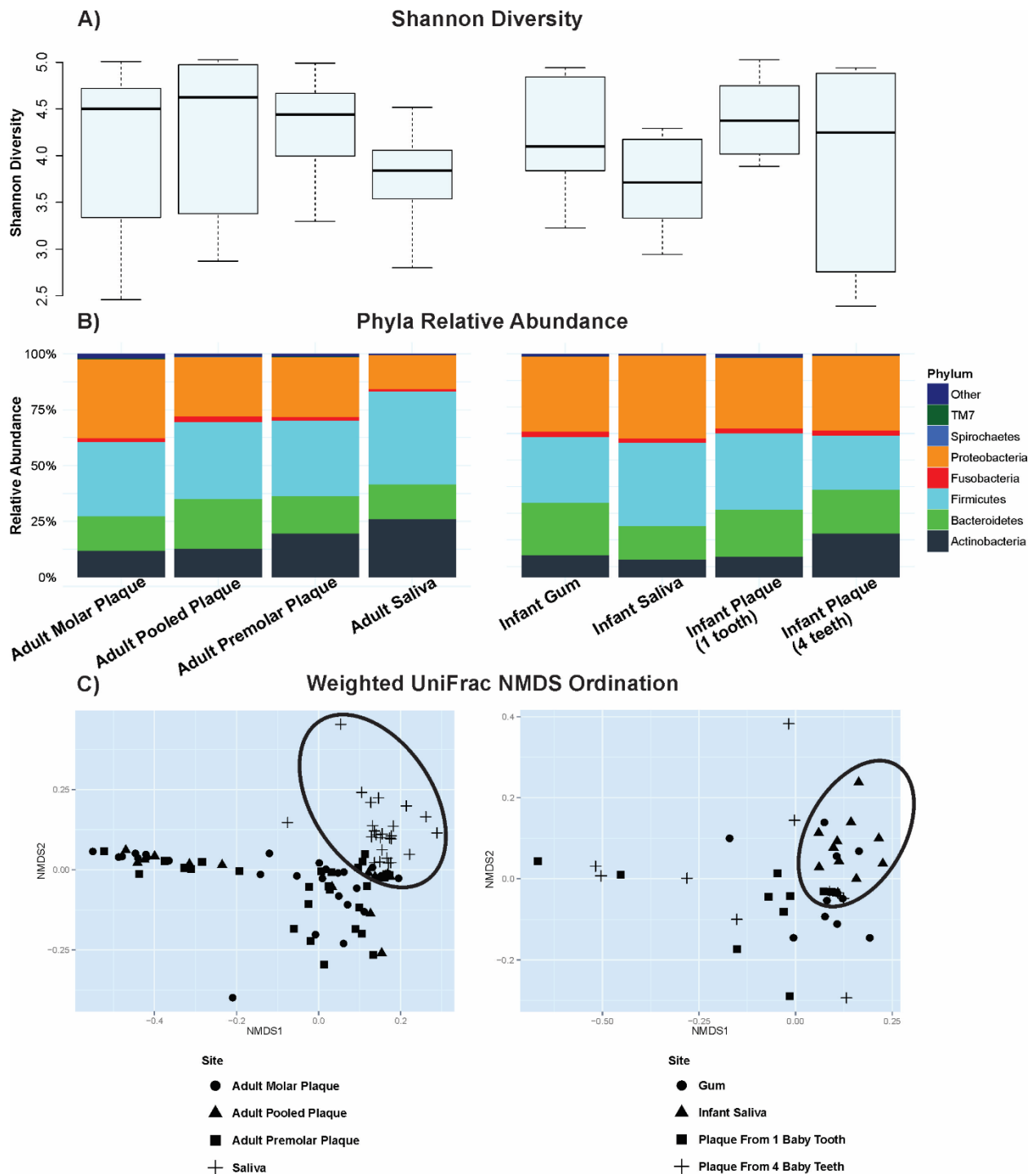**Supplemental Figures and Tables**

Figure S1: **Non-metric multidimensional scaling ordination plots of oral specimens.**

NMDS plot of all adult plaque, adult saliva, and infant samples. (A) Microbial communities recovered from adult plaque collected using dental scaler cannot be visually distinguished from microbial communities recovered from adult plaque collected using CytoSoft™. (B and C) Microbial communities recovered from adult plaque/saliva stored in Omnigene™ were more similar than microbial communities recovered from adult plaque/saliva stored in LDTM.
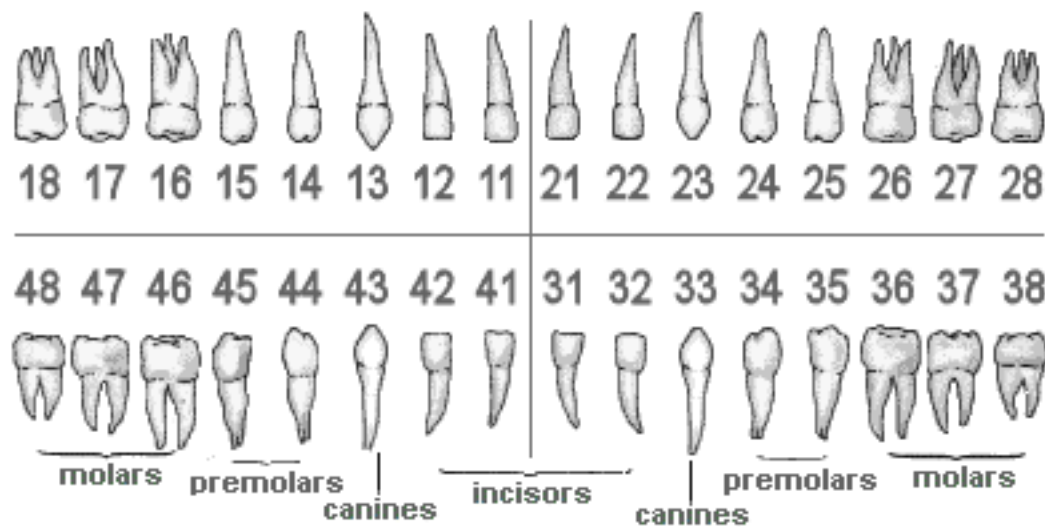
Figure S2: **Various ecological outcomes by oral site**.

Shannon index, phyla relative abundance, and weighted UniFrac ordination plots comparing 4 sites amongst 4 adults and 6 infants. (A) Microbial communities recovered from adult and infant

saliva were less diverse than communities recovered from plaque and in the instance of infants,

gum as well. (B) Composition at the phyla level shows minimal differences between oral sites.

(C) In both adults and infants, microbial communities recovered from saliva can be visually

distinguished from microbial communities recovered from plaque and gum.
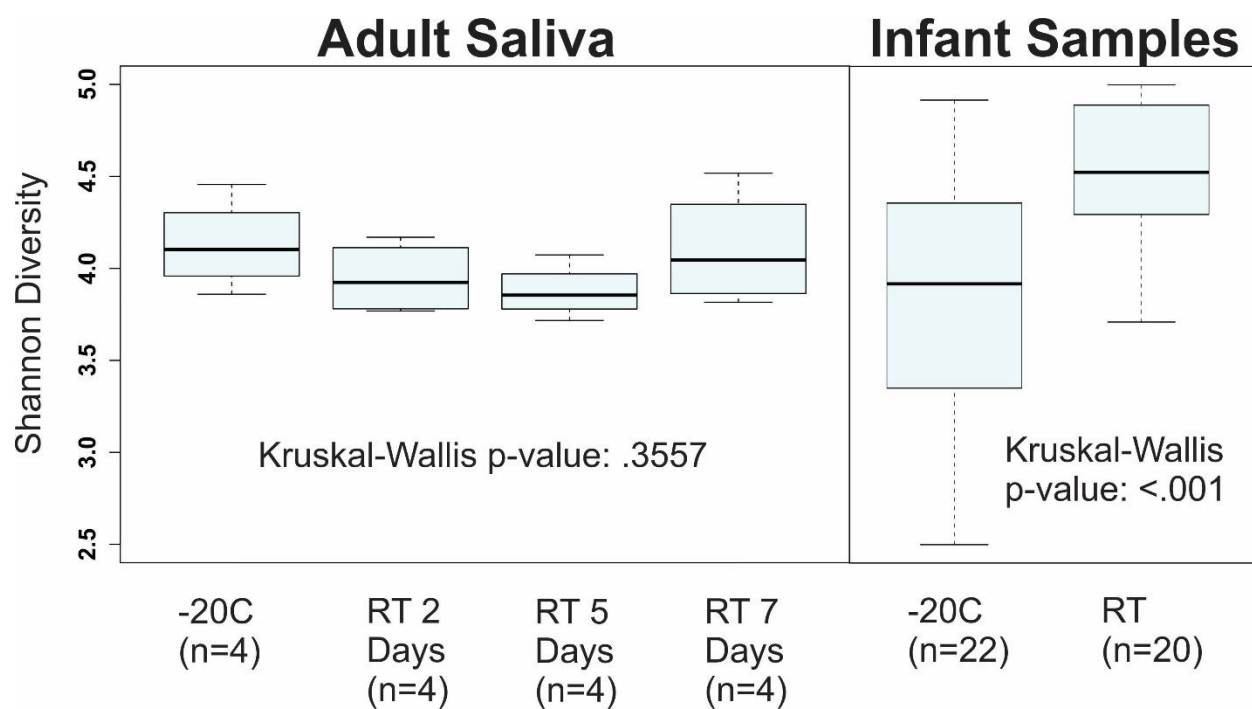
Figure S3: Map of teeth sampled according to collection schedule.

Map of oral cavity indicating which teeth are sampled according to collection schedule (Table 1).

Adult molars sampled include 16, 17, 26, 27, 36, 37, 46, and 47. Adult premolars sampled 14,

15, 24, 25, 34, 35, 44 and 45.

Figure S4: **The effects of storage temperature on adult saliva and infant samples stored in**
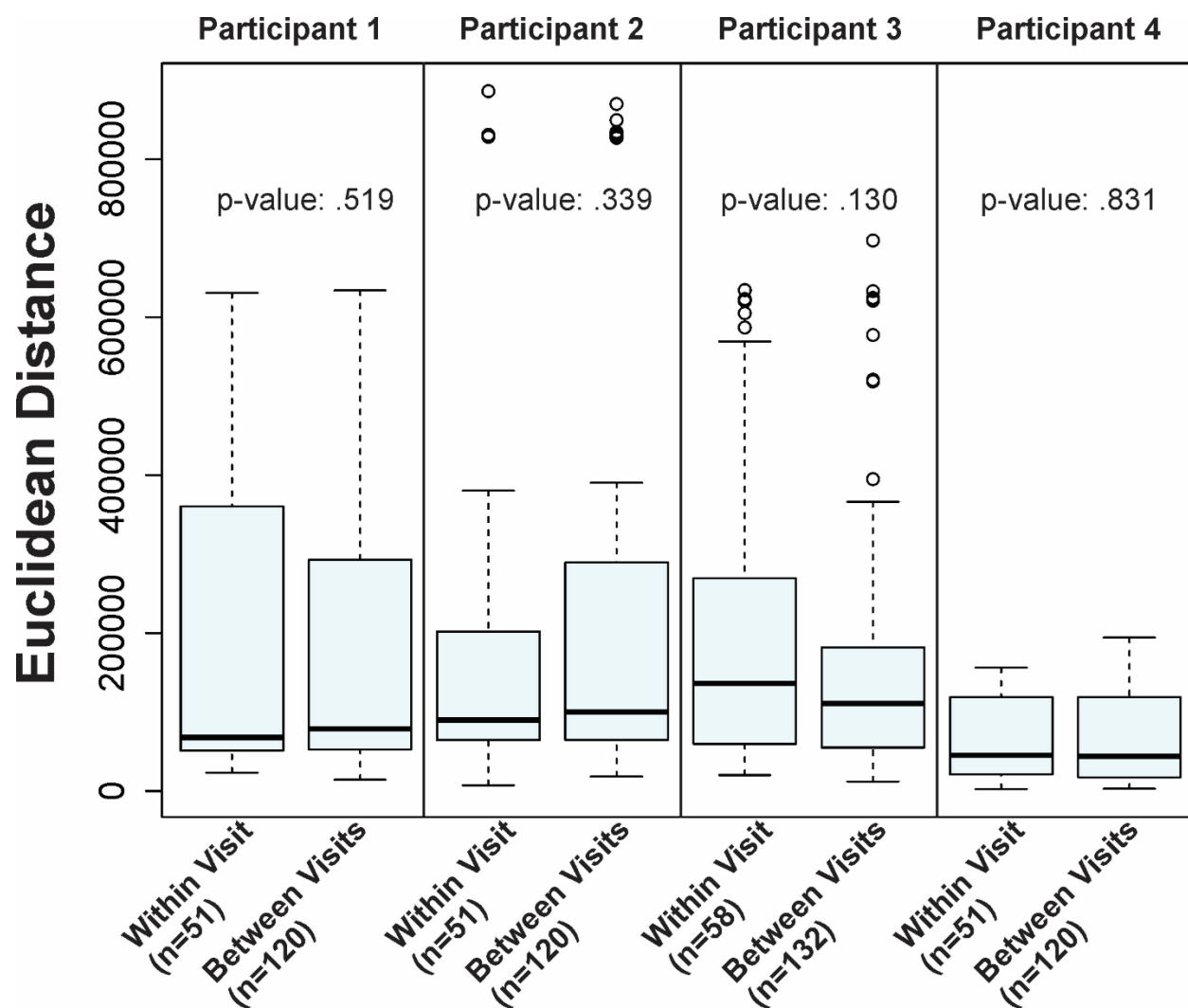
Omnigene™

Shannon index of adult saliva and infant samples stored in Omnigene™ by storage conditions. Storage conditions have no effect on the Shannon alpha diversity outcome of adult saliva samples. Room temperature storage of infant samples yielded higher Shannon alpha diversity compared to infant samples stored at -20C.

Figure S5: **The short-term stability of adult plaque samples by participant**

The Euclidean distance between plaque samples within participant visit and between participant visit. The average Euclidean distance between plaque samples from a participant collected on the same day cannot be distinguished from the average Euclidean distance between plaque samples from a participant collected different days. Each participant recorded 4 visits over 2 weeks (Table 1). For all 4 participants, plaque microbial communities remained stable over 2 weeks.

Table S1: Mock Community Constituents

Actinomyces naeslundii	Lactobacillus animalis	Lactobacillus salivarius
Atopobium rimae	Lactobacillus brevis	Lactobacillus vaginalis
Atopobium vaginae	Lactobacillus buchneri	Lactobacillus zeae
Bifidobacterium catnelatum	Lactobacillus casei	Lactobacillusacidipiscis
Gardnerella vaginalis	Lactobacillus crispatus	Megasphera elsdenii
Mobiluncus curtisii	Lactobacillus curvatus	Parvimonas micra
Mobiluncus mulieris	Lactobacillus diolivorans	Pediococcus acidilactici
Capnocytophaga ochracea	Lactobacillus fermentum	Peptoniphilus asaccharolyticus
Capnocytophaga sputigena	Lactobacillus gallinarum	Peptoniphilus irvorii
Porphyromonas asaccharolytica	Lactobacillus gasseri	Peptoniphilus lacrimalis
Porphyromonas gingivalis	Lactobacillus iners	Peptostreptococcus anaerobius
Prevotella bivia	Lactobacillus intestinalis	Staphyloccocus aureus
Prevotella buccalis	Lactobacillus jensenii	Streptococcus agalactiae
Prevotella intermedia	Lactobacillus johnsonii	Campylobacter gracilis
Prevotella negrescens	Lactobacillus kefiri	Campylobacter rectus
Tannerella forsythia	Lactobacillus paracasei	Escherichia coli
Anaerococcus prevotii	Lactobacillus reuteri	Mycoplasma sp.
Finegoldia magna	Lactobacillus rhamnosis	Mycoplasma hominis
Lactobacillus acidophilus	Lactobacillus ruminus	Ureaplasma urealyitcus

Table listing the 57 strains that constitute the mock community.

Table S2: Expected and Observed Phyla and Genera Relative Abundances of Mock Community

Genera	Expected Genera Relative Abundance	Observed Genera Relative Abundance
Actinomyces	0.02	0
Anaerococcus	0.02	0.02
Atopobium	0.04	0.01
Bifidobacterium	0.02	0.02
Campylobacter	0.04	0
Capnocytophaga	0.04	0.01
Escherichia	0.02	0
Finegoldia	0.02	0.02
Gardnerella	0.02	0
Lactobacillus	0.42	0.29
Megasphera	0.02	0.06
Mobiluncus	0.04	0
Mycoplasma	0.04	0
Parvimonas	0.02	0
Pediococcus	0.02	0
Peptoniphilus	0.05	0.12
Peptostreptococcus	0.02	0.02
Porphyromonas	0.04	0.02
Prevotella	0.07	0.04
Staphyloccocus	0.02	0.04
Streptococcus	0.02	0.02
Tannerella	0.02	0.02
Ureaplasma	0.02	0
Other	0	0.29
Phyla	**Expected Phyla Abundance**	**Observed Phyla Relative Abundance**
Actinobacteria	0.12	0.26
Bacteroidetes	0.16	0.08
Firmicutes	0.61	0.63
Proteobacteria	0.05	0.03
Tenericutes	0.05	0

DNA extracted from each strain were normalized to 3 ng/uL and 3 ng of each strain was used to create the mock community. Phyla and genera expected relative abundances were calculated

based on the mock community composition. Sequences with mock community barcodes were extracted and assigned OTUs using GreenGenes 13.8 as a reference database. The taxonomic assignments from the resultant OTU table was then used to construct observed relative abundance of phyla and genera.